

			290							295			
Gly	Phe	Asp	Thr	Asn	Gln	Glu	Ile	Phe	Gln	Glu	Leu	Ser	
300					305					310			
Arg	Gly	Leu	Pro	Thr	Gly	Gln	Ala	Gln	Val	Ala	Val	His	
		315					320					325	
Cys	Leu	Lys	Val	Pro	Lys	Ile	Ser	Cys	Gln	Asn	Arg	Gly	
				330					335				
Val	Val	Val	Ser	Ser	Ser	Val	Ala	Val	Thr	Phe	Arg	Phe	
	340					345					350		
Pro	Arg	Pro	Asp	Gly	Arg	Glu	Ala	Val	Ala	Tyr	Arg	Phe	
			355						360				
Glu	Glu	Asp	Ile	Ile	Thr	Thr	Val	Gln	Ala	Ser	Tyr	Ser	
365					370					375			
Gln	Lys	Lys	Leu	Phe	Leu	His	Leu	Leu	Asp	Phe	Gln	Cys	
		380					385					390	
Val	Pro	Ala	Ser	Gly	Arg	Ala	Gly	Ser	Ser	Ala	Asn	Leu	
				395						400			
Ser	Val	Ala	Leu	Arg	Thr	Glu	Ala	Lys	Ala	Val	Ser	Asn	
	405					410					415		
Leu	Thr	Glu	Ser	Arg	Ser	Glu	Ser	Leu	Gln	Ser	Ser	Leu	
			420						425				
Arg	Ser	Leu	Ile	Ala	Thr	Val	Gly	Ile	Pro	Glu	Val	Met	
430					435					440			
Ser	Arg	Leu	Glu	Val	Ala	Phe	Thr	Ala	Leu	Met	Asn	Ser	
		445					450					455	
Lys	Gly	Leu	Asp	Leu	Phe	Glu	Ile	Ile	Asn	Pro	Glu	Ile	
				460					465				
Ile	Thr	Leu	Asp	Gly	Cys	Leu	Leu	Leu	Gln	Met	Asp	Phe	
	470					475					480		
Gly	Phe	Pro	Lys	His	Leu	Leu	Val	Asp	Phe	Leu	Gln	Ser	
			485					490					
Leu	Ser												
495													

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- (2) INFORMATION FOR SEQ ID NO: 3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:
 - (A) NAME: Structural coding sequence for mature human CETP
 - (B) LOCATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Drayna, Dennis, et al.
 - (B) TITLE: Cloning and sequencing of human cholesteryl ester transfer cDNA
 - (C) JOURNAL: Nature
 - (D) VOLUME: 327
 - (E) ISSUE:
 - (F) PAGES: 632 - 634
 - (G) DATE: 18-JUN-1987
 - (K) RELEVANT RESIDUES IN SEQ ID NO:3: FROM 1 TO 1428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

TGCTCCAAAG GCACCTCGCA CGAGGCAGGC ATCGTGTGCC GCATCACCAA      50
GCCTGCCCTC CTGGTGTGTA ACCACGAGAC TGCCAAGGTG ATCCAGACCG      100
CCTTCCAGCG AGCCAGCTAC CCAGATATCA CGGGCGAGAA GGCCATGATG      150
CTCCTTGGCC AAGTCAAGTA TGGGTTGCAC AACATCCAGA TCAGCCACTT      200
GTCCATCGCC AGCAGCCAGG TGGAGCTGGT GGAAGCCAAG TCCATTGATG      250
TCTCCATTCA GAACGTGTCT GTGGTCTTCA AGGGGACCCT GAAGTATGGC      300
TACACCACTG CCTGGTGGCT GGGTATTGAT CAGTCCATTG ACTTCGAGAT      350
CGACTCTGCC ATTGACCTCC AGATCAACAC ACAGCTGACC TGTGACTCTG      400
GTAGAGTGCG GACCGATGCC CCTGACTGCT ACCTGTCTTT CCATAAGCTG      450
CTCCTGCATC TCCAAGGGGA GCGAGAGCCT GGGTGGATCA AGCAGCTGTT      500
CACAAATTTT ATCTCCTTCA CCCTGAAGCT GGTCCTGAAG GGACAGATCT      550
GCAAAGAGAT CAACGTCATC TCTAACATCA TGGCCGATTT TGTCCAGACA      600
AGGGCTGCCA GCATCCTTTC AGATGGAGAC ATTGGGGTGG ACATTTCCCT      650
GACAGGTGAT CCCGTCATCA CAGCCTCCTA CCTGGAGTCC CATCACAAAG      700
GTCATTTTCA CTACAAGAAT GTCTCAGAGG ACCTCCCCCT CCCCACCTTC      750
TCGCCCACAC TGCTGGGGGA CTCCCGCATG CTGTACTTCT GGTTCTCTGA      800
GCGAGTCTTC CACTCGCTGG CCAAGGTAGC TTTCCAGGAT GGCCGCCTCA      850
TGCTCAGCCT GATGGGAGAC GAGTTCAAGG CAGTGCTGGA GACCTGGGGC      900
  
```

The following information is provided for informational purposes only.

```

TTCAACACCA ACCAGGAAAT CTTCCAAGAG GTTGTCTGGCG GCTTCCCCAG    950
CCAGGCCCAA GTCACCGTCC ACTGCCTCAA GATGCCCAAG ATCTCCTGCC    1000
AAAACAAGGG AGTCGTGGTC AATTCTTCAG TGATGGTGAA ATTCCTCTTT    1050
CCACGCCCAG ACCAGCAACA TTCTGTAGCT TACACATTTG AAGAGGATAT    1100
CGTGACTACC GTCCAGGCCT CCTATTCTAA GAAAAAGCTC TTCTTAAGCC    1150
TCTTGGATTT CCAGATTACA CCAAAGACTG TTTCCAACTT GACTGAGAGC    1200
AGCTCCGAGT CCATCCAGAG CTTCTGCAG TCAATGATCA CCGCTGTGGG    1250
CATCCCTGAG GTCATGTCTC GGCTCGAGGT AGTGTTTACA GCCCTCATGA    1300
ACAGCAAAGG CGTGAGCCTC TTCGACATCA TCAACCCTGA GATTATCACT    1350
CGAGATGGCT TCCTGCTGCT GCAGATGGAC TTTGGCTTCC CTGAGCACCT    1400
GCTGGTGGAT TTCCTCCAGA GCTTGAGC                                1428
    
```

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 476 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:
 - (A) NAME: Amino acid sequence of mature human CETP
 - (B) LOCATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Drayna, Dennis, et al.
 - (B) TITLE: Cloning and sequencing of human cholesteryl ester transfer cDNA
 - (C) JOURNAL: Nature
 - (D) VOLUME: 327
 - (E) ISSUE:
 - (F) PAGES: 632 - 634
 - (G) DATE: 18-JUN-1987
 - (K) RELEVANT RESIDUES IN SEQ ID NO:4: FROM 1 TO 476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val Cys
1           5           10

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn His Glu
15           20           25

Thr Ala Lys Val Ile Gln Thr Ala Phe Gln Arg Ala Ser
    
```

The following sequence is a computer-generated sequence.

			30						35				
Tyr	Pro	Asp	Ile	Thr	Gly	Glu	Lys	Ala	Met	Met	Leu	Leu	
40					45					50			
Gly	Gln	Val	Lys	Tyr	Gly	Leu	His	Asn	Ile	Gln	Ile	Ser	
		55					60					65	
His	Leu	Ser	Ile	Ala	Ser	Ser	Gln	Val	Glu	Leu	Val	Glu	
				70					75				
Ala	Lys	Ser	Ile	Asp	Val	Ser	Ile	Gln	Asn	Val	Ser	Val	
	80					85					90		
Val	Phe	Lys	Gly	Thr	Leu	Lys	Tyr	Gly	Tyr	Thr	Thr	Ala	
			95					100					
Trp	Trp	Leu	Gly	Ile	Asp	Gln	Ser	Ile	Asp	Phe	Glu	Ile	
105					110					115			
Asp	Ser	Ala	Ile	Asp	Leu	Gln	Ile	Asn	Thr	Gln	Leu	Thr	
		120						125				130	
Cys	Asp	Ser	Gly	Arg	Val	Arg	Thr	Asp	Ala	Pro	Asp	Cys	
				135					140				
Tyr	Leu	Ser	Phe	His	Lys	Leu	Leu	Leu	His	Leu	Gln	Gly	
	145					150					155		
Glu	Arg	Glu	Pro	Gly	Trp	Ile	Lys	Gln	Leu	Phe	Thr	Asn	
			160					165					
Phe	Ile	Ser	Phe	Thr	Leu	Lys	Leu	Val	Leu	Lys	Gly	Gln	
170					175					180			
Ile	Cys	Lys	Glu	Ile	Asn	Val	Ile	Ser	Asn	Ile	Met	Ala	
		185					190					195	
Asp	Phe	Val	Gln	Thr	Arg	Ala	Ala	Ser	Ile	Leu	Ser	Asp	
				200					205				
Gly	Asp	Ile	Gly	Val	Asp	Ile	Ser	Leu	Thr	Gly	Asp	Pro	
	210					215					220		
Val	Ile	Thr	Ala	Ser	Tyr	Leu	Glu	Ser	His	His	Lys	Gly	
			225					230					
His	Phe	Ile	Tyr	Lys	Asn	Val	Ser	Glu	Asp	Leu	Pro	Leu	
235					240					245			
Pro	Thr	Phe	Ser	Pro	Thr	Leu	Leu	Gly	Asp	Ser	Arg	Met	
		250					255					260	
Leu	Tyr	Phe	Trp	Phe	Ser	Glu	Arg	Val	Phe	His	Ser	Leu	
				265					270				
Ala	Lys	Val	Ala	Phe	Gln	Asp	Gly	Arg	Leu	Met	Leu	Ser	
	275					280					285		

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Leu Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp
 290 295
 Gly Phe Asn Thr Asn Gln Glu Ile Phe Gln Glu Val Val
 300 305 310
 Gly Gly Phe Pro Ser Gln Ala Gln Val Thr Val His Cys
 315 320 325
 Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys Gly Val
 330 335
 Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro
 340 345 350
 Arg Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu
 355 360
 Glu Asp Ile Val Thr Thr Val Gln Ala Ser Tyr Ser Lys
 365 370 375
 Lys Lys Leu Phe Leu Ser Leu Leu Asp Phe Gln Ile Thr
 380 385 390
 Pro Lys Thr Val Ser Asn Leu Thr Glu Ser Ser Ser Glu
 395 400
 Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val
 405 410 415
 Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val Phe
 420 425
 Thr Ala Leu Met Asn Ser Lys Gly Val Ser Leu Phe Asp
 430 435 440
 Ile Ile Asn Pro Glu Ile Ile Thr Arg Asp Gly Phe Leu
 445 450 455
 Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu
 460 465
 Val Asp Phe Leu Gln Ser Leu Ser
 470 475

- (2) INFORMATION FOR SEQ ID NO: 5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE:
 - (iii) HYPOTHETICAL:
 - (iv) ANTI-SENSE:
 - (ix) FEATURE:

- (A) NAME:
- (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

GCGGCCGCCA TGCAGTACAT CAAGGCCAAC TCCAAGTTCA TCGGCATCAC    50
GGAGCGCTTC CCCC GCCCAG ATGGCCGAGA AGCTGTGGCC TACAGGTTTG    100
AGGAGGATAT CTTCGGTTTTT CCCAAGCACC TGCTGGTGGA TTTCTGCAG    150
AGCCTGAGCT AGCGGCCGC                                         169

```

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:
 - (A) NAME: Complementary strand to SEQ ID NO:5
 - (B) LOCATION: 1 to 169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

GCGGCCGCTA GCTCAGGCTC TGCAGGAAAT CCACCAGCAG GTGCTTGCGA    50
AAACCGAAGA TATCCTCCTC AAACCTGTAG GCCACAGCTT CTCGGCCATC    100
TGGGCGGGGG AAGCGCTCCG TGATGCCGAT GAACTTGGAG TTGGCCTTGA    150
TGTACTGCAT CGCGGCCGC                                         169

```

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE: amino acid sequence of peptide encoded by bases 10 to 159 of SEQ ID NO:5
 - (A) NAME:
 - (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile
1           5           10
Thr Glu Arg Phe Pro Arg Pro Asp Gly Arg Glu Ala Val
15           20           25

```

Ala Tyr Arg Phe Glu Glu Asp Ile Phe Gly Phe Pro Lys
 30 35

His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
 40 45 50

- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1608 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE:
 - (iii) HYPOTHETICAL:
 - (iv) ANTI-SENSE:
 - (ix) FEATURE:
 - (A) NAME: translational stop codon
 - (B) LOCATION: 1606 - 1608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCGCTGATG ATGTTGTTGA TTCTTCTAAA TCTTTTGTGA TGGAAAACCT 50
 TTCTTCGTAC CACGGGACTA AACCTGGTTA TGTAGATTCC ATTCAAAAAG 100
 GTATACAAAA GCCAAAATCT GGTACACAAG GAAATTATGA CGATGATTGG 150
 AAAGGGTTTT ATAGTACCGA CAATAAATAC GACGCTGCCG GATACTCTGT 200
 AGATAATGAA AACCCGCTCT CTGGAAAAGC TGGAGGCGTG GTCAAAGTGA 250
 CGTATCCAGG ACTGACGAAG GTTCTCGCAC TAAAAGTGG AATGCCGAA 300
 ACTATTAAGA AAGAGTTAGG TTTAAGTCTC ACTGAACCGT TGATGGAGCA 350
 AGTCGGAACG GAAGAGTTTA TCAAAAGGTT CGGTGATGGT GCTTCGCGTG 400
 TAGTGCTCAG CCTTCCCTTC GCTGAGGGGA GTTCTAGCGT TGAATATATT 450
 AATAACTGGG AACAGGCGAA AGCGTTAAGC GTAGAACTTG AGATTAATTT 500
 TGAAACCCGT GGAAAACGTG GCCAAGATGC GATGTATGAG TATATGGCTC 550
 AAGCCTGTGC AGGAAATCGT GTCAGGCGAT CAGTAGGTAG CTCATTGTCA 600

T C C A T T C A G G A C T G A C G A A G T T C T C G T G A A A A G C T G G A A A A C C T

AGTAGATCAC ACCAAGGTTA ATTCTAAGCT ATCGCTATTT TTTGAAATCA 1600

AAAGCTGA 1608

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 535 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:
 - (A) NAME:
 - (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly	Ala	Asp	Asp	Val	Val	Asp	Ser	Ser	Lys	Ser	Phe	Val	Met
1				5					10				
Glu	Asn	Phe	Ser	Ser	Tyr	His	Gly	Thr	Lys	Pro	Gly	Tyr	Val
15					20				25				
Asp	Ser	Ile	Gln	Lys	Gly	Ile	Gln	Lys	Pro	Lys	Ser	Gly	Thr
30					35						40		
Gln	Gly	Asn	Tyr	Asp	Asp	Asp	Trp	Lys	Gly	Phe	Tyr	Ser	Thr
		45					50					55	
Asp	Asn	Lys	Tyr	Asp	Ala	Ala	Gly	Tyr	Ser	Val	Asp	Asn	Glu
			60					65					70
Asn	Pro	Leu	Ser	Gly	Lys	Ala	Gly	Gly	Val	Val	Lys	Val	Thr
				75					80				
Tyr	Pro	Gly	Leu	Thr	Lys	Val	Leu	Ala	Leu	Lys	Val	Asp	Asn
85					90					95			
Ala	Glu	Thr	Ile	Lys	Lys	Glu	Leu	Gly	Leu	Ser	Leu	Thr	Glu
	100					105					110		
Pro	Leu	Met	Glu	Gln	Val	Gly	Thr	Glu	Glu	Phe	Ile	Lys	Arg
		115					120					125	
Phe	Gly	Asp	Gly	Ala	Ser	Arg	Val	Val	Leu	Ser	Leu	Pro	Phe
			130					135					140
Ala	Glu	Gly	Ser	Ser	Ser	Val	Glu	Tyr	Ile	Asn	Asn	Trp	Glu
				145					150				
Gln	Ala	Lys	Ala	Leu	Ser	Val	Glu	Leu	Glu	Ile	Asn	Phe	Glu
155					160					165			
Thr	Arg	Gly	Lys	Arg	Gly	Gln	Asp	Ala	Met	Tyr	Glu	Tyr	Met

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170						175						180	
Ala	Gln	Ala	Cys	Ala	Gly	Asn	Arg	Val	Arg	Arg	Ser	Val	Gly
		185					190					195	
Ser	Ser	Leu	Ser	Cys	Ile	Asn	Leu	Asp	Trp	Asp	Val	Ile	Arg
			200					205					210
Asp	Lys	Thr	Lys	Thr	Lys	Ile	Glu	Ser	Leu	Lys	Glu	His	Gly
				215					220				
Pro	Ile	Lys	Asn	Lys	Met	Ser	Glu	Ser	Pro	Asn	Lys	Thr	Val
225					230					235			
Ser	Glu	Glu	Lys	Ala	Lys	Gln	Tyr	Leu	Glu	Glu	Phe	His	Gln
	240					245					250		
Thr	Ala	Leu	Glu	His	Pro	Glu	Leu	Ser	Glu	Leu	Lys	Thr	Val
		255					260					265	
Thr	Gly	Thr	Asn	Pro	Val	Phe	Ala	Gly	Ala	Asn	Tyr	Ala	Ala
			270					275					280
Trp	Ala	Val	Asn	Val	Ala	Gln	Val	Ile	Asp	Ser	Glu	Thr	Ala
				285					290				
Asp	Asn	Leu	Glu	Lys	Thr	Thr	Ala	Ala	Leu	Ser	Ile	Leu	Pro
295					300					305			
Gly	Ile	Gly	Ser	Val	Met	Gly	Ile	Ala	Asp	Gly	Ala	Val	His
	310					315					320		
His	Asn	Thr	Glu	Glu	Ile	Val	Ala	Gln	Ser	Ile	Ala	Leu	Ser
		325					330					335	
Ser	Leu	Met	Val	Ala	Gln	Ala	Ile	Pro	Leu	Val	Gly	Glu	Leu
			340					345					350
Val	Asp	Ile	Gly	Phe	Ala	Ala	Tyr	Asn	Phe	Val	Glu	Ser	Ile
				355					360				
Ile	Asn	Leu	Phe	Gln	Val	Val	His	Asn	Ser	Tyr	Asn	Arg	Pro
365					370					375			
Ala	Tyr	Ser	Pro	Gly	His	Lys	Thr	Gln	Pro	Phe	Leu	His	Asp
	380					385					390		
Gly	Tyr	Ala	Val	Ser	Trp	Asn	Thr	Val	Glu	Asp	Ser	Ile	Ile
		395					400					405	
Arg	Thr	Gly	Phe	Gln	Gly	Glu	Ser	Gly	His	Asp	Ile	Lys	Ile
			410					415					420
Thr	Ala	Glu	Asn	Thr	Pro	Leu	Pro	Ile	Ala	Gly	Val	Leu	Leu
				425					430				
Pro	Thr	Ile	Pro	Gly	Lys	Leu	Asp	Val	Asn	Lys	Ser	Lys	Thr
435					440					445			

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His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg
 450 455 460

Ala Ile Asp Gly Asp Val Thr Phe Cys Arg Pro Lys Ser Pro
 465 470 475

Val Tyr Val Gly Asn Gly Val His Ala Asn Leu His Val Ala
 480 485 490

Phe His Arg Ser Ser Ser Glu Lys Ile His Ser Asn Glu Ile
 495 500

Ser Ser Asp Ser Ile Gly Val Leu Gly Tyr Gln Lys Thr Val
 505 510 515

Asp His Thr Lys Val Asn Ser Lys Leu Ser Leu Phe Phe Glu
 520 525 530

Ile Lys Ser
 535

- (2) INFORMATION FOR SEQ ID NO:10
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL:
 - (iv) ANTI-SENSE:
 - (ix) FEATURE:
 - (A) NAME:
 - (B) LOCATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro
 1 5 10

Lys Val Ser Ala Ser His Leu Glu
 15 20

PCT/US97/07294

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Thomas, Lawrence J.
- (ii) TITLE OF INVENTION: PLASMID-BASED VACCINE FOR
TREATING ATHEROSCLEROSIS
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Yankwich & Associates
(B) STREET: 130 Bishop Allen Drive
(C) CITY: Cambridge
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02139
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: Windows 95/98
(D) SOFTWARE: Word 97
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:(not yet assigned)
(B) FILING DATE: 30 April 2001
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION: 08/640,713
(B) FILING DATE: 01 May 1996 (01.05.96)
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION: 08/802,967
(B) FILING DATE: 21 February 1997 (21.02.97)
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION: 09/171,969
(B) FILING DATE: 29 October 1998 (29.10.98)
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Leon R. Yankwich
(B) REGISTRATION NUMBER: 30,237
(C) REFERENCE/DOCKET NUMBER: TCS-414.2 US-1

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cdna
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE: Structural coding sequence for

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mature rabbit CETP

- (A) NAME:
- (B) LOCATION:
- (x) PUBLICATION INFORMATION:
- (A) AUTHORS: Nagashima, Mariko, et al.
- (B) TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protein
- (C) JOURNAL: J. Lipid Res.
- (D) VOLUME: 29
- (E) ISSUE:
- (F) PAGES: 1643 - 1649
- (G) DATE: 1988
- (K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 1488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TGTCCCAAAG GCGCCTCCTA CGAGGCTGGC ATCGTGTGTC GCATCACCAA	50
GCCCGCCCTC TTGGTGTGA ACCAAGAGAC GGCCAAGGTG GTCCAGACGG	100
CCTTCAGCG CGCCGGCTAT CCGGACGTCA GCGGCGAGAG GGCCGTGATG	150
CTCCTCGGCC GGGTCAAGTA CGGGCTGCAC AACCTCCAGA TCAGCCACCT	200
GTCCATCGCC AGCAGCCAGG TGGAGCTGGT GGACGCCAAG ACCATCGACG	250
TCGCCATCCA GAACGTGTCC GTGGTCTTCA AGGGGACCCT GAACTACAGC	300
TACACGAGTG CCTGGGGGTT GGGCATCAAT CAGTCTGTCG ACTTCGAGAT	350
CGACTCTGCC ATTGACCTCC AGATCAACAC AGAGCTGACC TGCGACGCTG	400
GCAGTGTGCG CACCAATGCC CCCGACTGCT ACCTGGCTTT CCATAAACTG	450
CTCCTGCACC TCCAGGGGGA GCGCGAGCCG GGGTGGCTCA AGCAGCTCTT	500
CACAAACTTC ATCTCCTTCA CCCTGAAGCT GATTCTGAAG CGACAGGTCT	550
GCAATGAGAT CAACACCATC TCCAACATCA TGGCTGACTT TGTCCAGACG	600
AGGGCCGCCA GCATCCTCTC AGATGGAGAC ATCGGGGTGG ACATTTCCGT	650
GACGGGGGCC CCTGTCATCA CAGCCACCTA CCTGGAGTCC CATCACAAGG	700
GTCACCTCAC GCACAAGAAC GTCTCCGAGG CCTTCCCCCT CCGCGCCTTC	750
CCGCCCCGGTCTTCTGGGGGA CTCCCGCATG CTCTACTTCT GGTTCCTCCGA	800
TCAAGTGCTC AACTCCCTGG CCAGGGCCGC CTTCCAGGAG GGCCGTCTCG	850
TGCTCAGCCT GACAGGGGAT GAGTTCAAGA AAGTGCTGGA GACCCAGGGT	900
TTCGACACCA ACCAGGAAAT CTTCCAGGAG CTTTCCAGAG GCCTTCCCAC	950
CGGCCAGGCC CAGGTAGCCG TCCACTGCCT TAAGGTGCCC AAGATCTCCT	1000

CGCGCCCTTC

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GCCAGAACCG GGGTGTTCGTG GTGTCTTCTT CCGTCGCCGT GACGTTCCGC      1050
TTCCCCCGCC CAGATGGCCG AGAAGCTGTG GCCTACAGGT TTGAGGAGGA      1100
TATCATCACC ACCGTCCAGG CCTCCTACTC CCAGAAAAG CTCTTCCTAC      1150
ACCTCTTGGA TTTCCAGTGC GTGCCGGCCA GCGGAAGGGC AGGCAGCTCA      1200
GCAAATCTCT CCGTGGCCCT CAGGACTGAG GCTAAGGCTG TTTCCAACCT      1250
GACTGAGAGC CGTCCGAGT CCCTGCAGAG CTCTCTCCGC TCCCTGATCG      1300
CCACGGTGGG CATCCCGAG GTCATGTCTC GGCTCGAGGT GGCCTTCACA      1350
GCCCTCATGA ACAGCAAAGG CCTGGACCTC TTCGAAATCA TCAACCCCGA      1400
GATTATCACT CTCGATGGCT GCCTGCTGCT GCAGATGGAC TTCGGTTTTTC      1450
CCAAGCACCT GCTGGTGGAT TTCCTGCAGA GCCTGAGC                      1488

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 496 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:

(A) NAME: Amino acid sequence for mature rabbit CETP protein.
(B) LOCATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Nagashima, Mariko, et al.
(B) TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protein

(C) JOURNAL: J. Lipid Res.
(D) VOLUME: 29
(E) ISSUE:
(F) PAGES: 1643 - 1649
(G) DATE: 1988
(K) RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Cys Pro Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys
1 5 10

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn Gln Glu
15 20 25

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Thr Ala Lys Val Val Gln Thr Ala Phe Gln Arg Ala Gly
30 35

Tyr Pro Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu
40 45 50

Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile Ser
55 60 65

His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp
70 75

Ala Lys Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val
80 85 90

Val Phe Lys Gly Thr Leu Asn Tyr Ser Tyr Thr Ser Ala
95 100

Trp Gly Leu Gly Ile Asn Gln Ser Val Asp Phe Glu Ile
105 110 115

Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu Leu Thr
120 125 130

Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys
135 140

Tyr Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly
145 150 155

Glu Arg Glu Pro Gly Trp Leu Lys Gln Leu Phe Thr Asn
160 165

Phe Ile Ser Phe Thr Leu Lys Leu Ile Leu Lys Arg Gln
170 175 180

Val Cys Asn Glu Ile Asn Thr Ile Ser Asn Ile Met Ala
185 190 195

Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
200 205

Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro
210 215 220

Val Ile Thr Ala Thr Tyr Leu Glu Ser His His Lys Gly
225 230

His Phe Thr His Lys Asn Val Ser Glu Ala Phe Pro Leu
235 240 245

Arg Ala Phe Pro Pro Gly Leu Leu Gly Asp Ser Arg Met
250 255 260

Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser Leu

265

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Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser
275 280 285

Leu Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln
290 295

Gly Phe Asp Thr Asn Gln Glu Ile Phe Gln Glu Leu Ser
300 305 310

Arg Gly Leu Pro Thr Gly Gln Ala Gln Val Ala Val His
315 320 325

Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn Arg Gly
330 335

Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe
340 345 350

Pro Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe
355 360

Glu Glu Asp Ile Ile Thr Thr Val Gln Ala Ser Tyr Ser
365 370 375

Gln Lys Lys Leu Phe Leu His Leu Leu Asp Phe Gln Cys
380 385 390

Val Pro Ala Ser Gly Arg Ala Gly Ser Ser Ala Asn Leu
395 400

Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser Asn
405 410 415

Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu
420 425

Arg Ser Leu Ile Ala Thr Val Gly Ile Pro Glu Val Met
430 435 440

Ser Arg Leu Glu Val Ala Phe Thr Ala Leu Met Asn Ser
445 450 455

Lys Gly Leu Asp Leu Phe Glu Ile Ile Asn Pro Glu Ile
460 465

Ile Thr Leu Asp Gly Cys Leu Leu Gln Met Asp Phe
470 475 480

Gly Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser
485 490

Leu Ser
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- (2) INFORMATION FOR SEQ ID NO: 3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cdNA
 - (iii) HYPOTHETICAL:
 - (iv) ANTI-SENSE:
 - (ix) FEATURE:
 - (A) NAME: Structural coding sequence for mature human CETP
 - (B) LOCATION:
 - (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Drayna, Dennis, et al.
 - (B) TITLE: Cloning and sequencing of human cholesteryl ester transfer cDNA
 - (C) JOURNAL: Nature
 - (D) VOLUME: 327
 - (E) ISSUE:
 - (F) PAGES: 632 - 634
 - (G) DATE: 18-JUN-1987
 - (K) RELEVANT RESIDUES IN SEQ ID NO:3: FROM 1 TO 1428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGCTCAAAG GCACCTCGCA CGAGGCAGGC ATCGTGTGCC GCATCACCAA	50
GCCTGCCCTC CTGGTGTGA ACCACGAGAC TGCCAAGGTG ATCCAGACCG	100
CCTTCCAGCG AGCCAGCTAC CCAGATATCA CGGGCGAGAA GGCCATGATG	150
CTCCTTGGCC AAGTCAAGTA TGGGTTCAC AACATCCAGA TCAGCCACTT	200
GTCCATCGCC AGCAGCCAGG TGGAGCTGGT GGAAGCCAAG TCCATTGATG	250
TCTCCATTCA GAACGTGTCT GTGGTCTTCA AGGGGACCCT GAAGTATGGC	300
TACACCACTG CCTGGTGGCT GGGTATTGAT CAGTCCATTG ACTTCGAGAT	350
CGACTCTGCC ATTGACCTCC AGATCAACAC ACAGCTGACC TGTGACTCTG	400
GTAGAGTGCG GACCGATGCC CCTGACTGCT ACCTGTCTTT CCATAAGCTG	450
CTCCTGCATC TCCAAGGGGA GCGAGAGCCT GGGTGGATCA AGCAGCTGTT	500
CACAAATTTT ATCTCCTTCA CCCTGAAGCT GGTCCCTGAAG GGACAGATCT	550
GCAAAGAGAT CAACGTCATC TCTAACATCA TGGCCGATTT TGTCCAGACA	600
AGGGCTGCCA GCATCCTTTC AGATGGAGAC ATTGGGGTGG ACATTTCCCT	650
GACAGGTGAT CCCGTCATCA CAGCCTCCTA CCTGGAGTCC CATCACAAGG	700
GTCATTTTAT CTACAAGAAT GTCTCAGAGG ACCTCCCCCT CCCACCTTC	750

TCGCCACAC TGCTGGGGGA CTCCCAGCATG CTGTACTTCT GGTTCCTCTGA

TCGCCACAC TGCTGGGGGA CTCCCAGCATG CTGTACTTCT GGTTCCTCTGA	800
GCGAGTCTTC CACTCGCTGG CCAAGGTAGC TTTCCAGGAT GGCCGCCTCA	850
TGCTCAGCCT GATGGGAGAC GAGTTCAAGG CAGTGCTGGA GACCTGGGGC	900
TTCAACACCA ACCAGGAAAT CTTCCAAGAG GTTGTGCGGCG GCTTCCCAG	950
CCAGGCCCAA GTCACCGTCC ACTGCCTCAA GATGCCCAAG ATCTCCTGCC	1000
AAAACAAGGG AGTCGTGGTC AATTCTTCAG TGATGGTGAA ATTCCTCTTT	1050
CCACGCCAG ACCAGCAACA TTCTGTAGCT TACACATTTG AAGAGGATAT	1100
CGTGACTACC GTCCAGGCCT CCTATTCTAA GAAAAAGCTC TTCTTAAGCC	1150
TCTTGATTT CCAGATTACA CCAAAGACTG TTTCCAACCTT GACTGAGAGC	1200
AGCTCCGAGT CCATCCAGAG CTTCCTGCAG TCAATGATCA CCGCTGTGGG	1250
CATCCCTGAG GTCATGTCTC GGCTCGAGGT AGTGTTTACA GCCCTCATGA	1300
ACAGCAAAGG CGTGAGCCTC TTCGACATCA TCAACCCTGA GATTATCACT	1350
CGAGATGGCT TCCTGCTGCT GCAGATGGAC TTTGGCTTCC CTGAGCACCT	1400
GCTGGTGGAT TTCCTCCAGA GCTTGAGC	1428

- (2) INFORMATION FOR SEQ ID NO: 4:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:
 - (A) NAME: Amino acid sequence of mature human

- CETP
- (B) LOCATION:
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Drayna, Dennis, et al.
 - (B) TITLE: Cloning and sequencing of human cholesteryl ester transfer cDNA
 - (C) JOURNAL: Nature
 - (D) VOLUME: 327
 - (E) ISSUE:
 - (F) PAGES: 632 - 634
 - (G) DATE: 18-JUN-1987
 - (K) RELEVANT RESIDUES IN SEQ ID NO:4: FROM 1 TO 476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val Cys
1 5 10
Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn His Glu
15 20 25
Thr Ala Lys Val Ile Gln Thr Ala Phe Gln Arg Ala Ser
30 35
Tyr Pro Asp Ile Thr Gly Glu Lys Ala Met Met Leu Leu
40 45 50
Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln Ile Ser
55 60 65
His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Glu
70 75
Ala Lys Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val
80 85 90
Val Phe Lys Gly Thr Leu Lys Tyr Gly Tyr Thr Thr Ala
95 100
Trp Trp Leu Gly Ile Asp Gln Ser Ile Asp Phe Glu Ile
105 110 115
Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Gln Leu Thr
120 125 130
Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys
135 140
Tyr Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly
145 150 155
Glu Arg Glu Pro Gly Trp Ile Lys Gln Leu Phe Thr Asn
160 165
Phe Ile Ser Phe Thr Leu Lys Leu Val Leu Lys Gly Gln
170 175 180
Ile Cys Lys Glu Ile Asn Val Ile Ser Asn Ile Met Ala
185 190 195
Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
200 205
Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro
210 215 220
Val Ile Thr Ala Ser Tyr Leu Glu Ser His His Lys Gly
225 230
His Phe Ile Tyr Lys Asn Val Ser Glu Asp Leu Pro Leu
235 240 245

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Pro Thr Phe Ser Pro Thr Leu Leu Gly Asp Ser Arg Met
250 255 260

Leu Tyr Phe Trp Phe Ser Glu Arg Val Phe His Ser Leu
265 270

Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met Leu Ser
275 280 285

Leu Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp
290 295

Gly Phe Asn Thr Asn Gln Glu Ile Phe Gln Glu Val Val
300 305 310

Gly Gly Phe Pro Ser Gln Ala Gln Val Thr Val His Cys
315 320 325

Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys Gly Val
330 335

Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro
340 345 350

Arg Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu
355 360

Glu Asp Ile Val Thr Thr Val Gln Ala Ser Tyr Ser Lys
365 370 375

Lys Lys Leu Phe Leu Ser Leu Leu Asp Phe Gln Ile Thr
380 385 390

Pro Lys Thr Val Ser Asn Leu Thr Glu Ser Ser Ser Glu
395 400

Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val
405 410 415

Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val Phe
420 425

Thr Ala Leu Met Asn Ser Lys Gly Val Ser Leu Phe Asp
430 435 440

Ile Ile Asn Pro Glu Ile Ile Thr Arg Asp Gly Phe Leu
445 450 455

Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu
460 465

Val Asp Phe Leu Gln Ser Leu Ser
470 475

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:
- (A) NAME:
- (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGCCGCCA TGCAGTACAT CAAGGCCAAC TCCAAGTTCA TCGGCATCAC	50
GGAGCGCTTC CCCCGCCAG ATGGCCGAGA AGCTGTGGCC TACAGGTTTG	100
AGGAGGATAT CTTCGGTTTT CCCAAGCACC TGCTGGTGA TTTCTGCAG	150
AGCCTGAGCT AGCGCCGC	169

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE:
- (A) NAME: Complementary strand to SEQ ID NO:5
- (B) LOCATION: 1 to 169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGGCCGCTA GCTCAGGCTC TGCAGGAAAT CCACCAGCAG GTGCTTGGGA	50
AAACCGAAGA TATCCTCCTC AAACCTGTAG GCCACAGCTT CTCGGCCATC	100
TGGGCGGGGG AAGCGCTCCG TGATGCCGAT GAACTTGGAG TTGGCCTTGA	150
TGTACTGCAT CGCGCCGC	169

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL:
- (iv) ANTI-SENSE:
- (ix) FEATURE: amino acid sequence of peptide encoded
by bases 10 to 159 of SEQ ID NO:5

- (A) NAME:
- (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile
 1 5 10

Thr Glu Arg Phe Pro Arg Pro Asp Gly Arg Glu Ala Val
 15 20 25

Ala Tyr Arg Phe Glu Glu Asp Ile Phe Gly Phe Pro Lys
 30 35

His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
 40 45 50

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(ix) FEATURE:

(A) NAME: translational stop codon

(B) LOCATION: 1606 - 1608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCGCTGATG ATGTTGTTGA TTCTTCTAAA TCTTTTGTGA TGGAAAACCT 50
 TTCTTCGTAC CACGGGACTA AACCTGGTTA TG TAGATTCC ATTCAAAAAG 100
 GTATACAAA GCCAAAATCT GGTACACAAG GAAATTATGA CGATGATTGG 150
 AAAGGGTTTT ATAGTACCGA CAATAAATAC GACGCTGCCG GATACTCTGT 200
 AGATAATGAA AACCCGCTCT CTGGAAAAGC TGGAGGCGTG GTCAAAGTGA 250
 CGTATCCAGG ACTGACGAAG GTTCTCGCAC TAAAAGTGA TAATGCCGAA 300
 ACTATTAAGA AAGAGTTAGG TTTAAGTCTC ACTGAACCGT TGATGGAGCA 350
 AGTCGGAACG GAAGAGTTTA TCAAAGGTT CGGTGATGGT GCTTCGCGTG 400
 TAGTGCTCAG CCTTCCCTTC GCTGAGGGGA GTTCTAGCGT TGAATATATT 450
 AATAACTGGG AACAGGCGAA AGCGTTAAGC GTAGAACTTG AGATTAATTT 500
 TGAAACCCGT GGAAAACGTG GCCAAGATGC GATGTATGAG TATATGGCTC 550
 AAGCCTGTGC AGGAAATCGT GTCAGGCGAT CAGTAGGTAG CTCATTGTCA 600

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TGCATAAATC TTGATTGGGA TGTCATAAGG GATAAAACTA AGACAAAGAT 650
AGAGTCTTTG AAAGAGCATG GCCCTATCAA AAATAAAATG AGCGAAAGTC 700
CCAATAAAAC AGTATCTGAG GAAAAAGCTA AACCAATACCT AGAAGAATTT 750
CATCAAACGG CATTAGAGCA TCCTGAATTG TCAGAACTTA AAACCGTTAC 800
TGGGACCAAT CCTGTATTCG CTGGGGCTAA CTATGCGGCG TGGGCAGTAA 850
ACGTTGCGCA AGTTATCGAT AGCGAAACAG CTGATAATTT GGAAAAGACA 900
ACTGCTGCTC TTTGATACT TCCTGGTATC GGTAGCGTAA TGGGCATTGC 950
AGACGGTGCC GTTCACCACA ATACAGAAGA GATAGTGGCA CAATCAATAG 1000
CTTTATCGTC TTTAATGGTT GCTCAAGCTA TTCCATTGGT AGGAGAGCTA 1050
GTTGATATTG GTTTCGCTGC ATATAATTTT GTAGAGAGTA TTATCAATTT 1100
ATTTCAAGTA GTTCATAAAT CGTATAATCG TCCCGCGTAT TCTCCGGGGC 1150
ATAAAACGCA ACCATTTCTT CATGACGGGT ATGCTGTCAG TTGGAACACT 1200
GTTGAAGATT CGATAATCCG AACTGGTTTT CAAGGGGAGA GTGGGCACGA 1250
CATAAAAATT ACTGCTGAAA ATACCCCGCT TCCAATCGCG GGTGTCCTAC 1300
TACCGACTAT TCCTGGAAAG CTGGACGTTA ATAAGTCCAA GACTCATATT 1350
TCCGTAAATG GTCGGAAAAT AAGGATGCGT TGCAGAGCTA TAGACGGTGA 1400
TGTAACTTTT TGTCGCCCTA AATCTCCTGT TTATGTTGGT AATGGTGTGC 1450
ATGCGAATCT TCACGTGGCA TTTACAGAA GCAGCTCGGA GAAAATTCAT 1500
TCTAATGAAA TTTCGTCGGA TTCCATAGGC GTTCTTGGGT ACCAGAAAAC 1550
AGTAGATCAC ACCAAGGTTA ATTCTAAGCT ATCGCTATTT TTTGAAATCA 1600
AAAGCTGA 1608

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 535 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(ix) FEATURE:

(A) NAME:

(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met
1 5 10

Glu Asn Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val
15 20 25

Asp Ser Ile Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr
30 35 40

Gln Gly Asn Tyr Asp Asp Asp Trp Lys Gly Phe Tyr Ser Thr
45 50 55

Asp Asn Lys Tyr Asp Ala Ala Gly Tyr Ser Val Asp Asn Glu
60 65 70

Asn Pro Leu Ser Gly Lys Ala Gly Gly Val Val Lys Val Thr
75 80

Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val Asp Asn
85 90 95

Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
100 105 110

Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg
115 120 125

Phe Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe
130 135 140

Ala Glu Gly Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu
145 150

Gln Ala Lys Ala Leu Ser Val Glu Leu Glu Ile Asn Phe Glu
155 160 165

Thr Arg Gly Lys Arg Gly Gln Asp Ala Met Tyr Glu Tyr Met
170 175 180

Ala Gln Ala Cys Ala Gly Asn Arg Val Arg Arg Ser Val Gly
185 190 195

Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile Arg
200 205 210

Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly
215 220

Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val
225 230 235

Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln
240 245 250

Thr Ala Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val
255 260 265

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Thr Gly Thr Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala
270 275 280

Trp Ala Val Asn Val Ala Gln Val Ile Asp Ser Glu Thr Ala
285 290

Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser Ile Leu Pro
295 300 305

Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val His
310 315 320

His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser
325 330 335

Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu
340 345 350

Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile
355 360

Ile Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro
365 370 375

Ala Tyr Ser Pro Gly His Lys Thr Gln Pro Phe Leu His Asp
380 385 390

Gly Tyr Ala Val Ser Trp Asn Thr Val Glu Asp Ser Ile Ile
395 400 405

Arg Thr Gly Phe Gln Gly Glu Ser Gly His Asp Ile Lys Ile
410 415 420

Thr Ala Glu Asn Thr Pro Leu Pro Ile Ala Gly Val Leu Leu
425 430

Pro Thr Ile Pro Gly Lys Leu Asp Val Asn Lys Ser Lys Thr
435 440 445

His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg
450 455 460

Ala Ile Asp Gly Asp Val Thr Phe Cys Arg Pro Lys Ser Pro
465 470 475

Val Tyr Val Gly Asn Gly Val His Ala Asn Leu His Val Ala
480 485 490

Phe His Arg Ser Ser Ser Glu Lys Ile His Ser Asn Glu Ile
495 500

Ser Ser Asp Ser Ile Gly Val Leu Gly Tyr Gln Lys Thr Val
505 510 515

Asp His Thr Lys Val Asn Ser Lys Leu Ser Leu Phe Phe Glu
520 525 530

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANT: Thomas, Lawrence J.
 - (ii) TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
 - (iii) NUMBER OF SEQUENCES: 10
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Banner & Witcoff, Ltd.
 - (B) STREET: 75 State Street, Suite 2300
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-1807
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WordPerfect 6.1
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: (not yet assigned)
 - (B) FILING DATE: 01 May 1997 (01.05.97)
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION: 08/640,713
 - (B) FILING DATE: 01 May 1996 (01.05.96)
 - (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION: 08/802,967
 - (B) FILING DATE: 21 February 1997 (21.02.97)
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Leon R. Yankwich
 - (B) REGISTRATION NUMBER: 30,237
 - (C) REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
- (2) INFORMATION FOR SEQ ID NO: 1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL:
 - (iv) ANTI-SENSE:
 - (ix) FEATURE: Structural coding sequence for mature rabbit CETP
 - (A) NAME:
 - (B) LOCATION:
 - (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Nagashima, Mariko, et al.

TCS 414.1 PCT (05872)

TATCATCACC ACCGTCCAGG CCTCCTACTC CCAGAAAAAG CTCTTCCTAC 1150
 ACCTCTTGGA TTTCCAGTGC GTGCCGGCCA GCGGAAGGGC AGGCAGCTCA 1200
 GCAAATCTCT CCGTGGCCCT CAGGACTGAG GCTAAGGCTG TTTCCAACCT 1250
 GACTGAGAGC CGCTCCGAGT CCCTGCAGAG CTCTCTCCGC TCCCTGATCG 1300
 CCACGGTGGG CATCCCGGAG GTCATGTCTC GGCTCGAGGT GGCCTTACACA 1350
 GCCCTCATGA ACAGCAAAGG CCTGGACCTC TTCGAAATCA TCAACCCCGA 1400
 GATTATCACT CTCGATGGCT GCCTGCTGCT GCAGATGGAC TTCGGTTTTTC 1450
 CCAAGCACCT GCTGGTGGAT TTCCTGCAGA GCCTGAGC 1488

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(ix) FEATURE:

- (A) NAME: Amino acid sequence for mature rabbit CETP protein.

(B) LOCATION:

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Nagashima, Mariko, et al.
- (B) TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protein
- (C) JOURNAL: J. Lipid Res.
- (D) VOLUME: 29
- (E) ISSUE:
- (F) PAGES: 1643 - 1649
- (G) DATE: 1988
- (K) RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Cys Pro Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys
 1 5 10
 Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn Gln Glu
 15 20 25
 Thr Ala Lys Val Val Gln Thr Ala Phe Gln Arg Ala Gly
 30 35
 Tyr Pro Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu

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